OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: November 11, 2005, 20:16:49 ; Search time 3276 Seconds
                   6146.520 Million cell updates/sec

Title: US-10-628-432-32
Perfect score: 2859
Sequence: 1 MSQTGSHPGRGLAGRWLWGA.........DQLQDFNIPQAVDYKDDDDK 529

Searched: 34239544 seqs, 19032134700 residues
                   Listing first 45 summaries

Total number of hits satisfying chosen parameters: 68479088

Scoring table:
   BLOSUM62
   Xgapop   10.0 ; Xgapext   0.5
   Ygapop   10.0 ; Ygapext   0.5
   Fgapop   6.0 ; Fgapext   7.0
   Delop   6.0 ; Delext   7.0

Post-processing: Minimum Match 0%
                  Maximum Match 100%

Minimum DB seq length: 1
Maximum DB seq length: 2000000000
                  (without alignments)

Command line parameters:
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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -NORM=ext -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20 -MODE=LOCAL
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-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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   2: gb_est2:*
   3: gb_htc:*
   4: gb_est3:*
   5: gb_est4:*
   6: gb_est5:*
   7: gb_est6:*
   8: gb_gss1:*
   9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match Length	DB ID	ID	Description
	1	2805	98.1	2514	9	AY404850 Homo sapi
	2	2774	97.0	2514	9	AY404851 Pan trog1
	3	2460	86.0	3673	3	AK083534 Mus muscu
	4	2459	86.0	2502	9	AY404852 Mus muscu
	5	2447	85.6	4390	3	AK028364 Mus muscu
	6	1638	57.3	3025	3	AK076295 Mus muscu
	7	1362.5	47.7	845	5	CD619814 56070459J
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	No.	Score	%	Match Len	DB	ID	Description
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c	13	1008	35.3	598	6	BM069515	1e88g09.x
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	15	952	33.3	590	6	CD619809	56070335H
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	18	885.5	31.0	882	5	CK412419	AUF_Ip61l
	19	877	30.7	840	5	BU214006	60749503
c	20	854.5	29.9	932	7	CA788933	AGENCOURT
	21	841	29.4	736	7	CF734236	UI-M-HB0-
	22	835	29.2	531	9	OST152925	OST152925
c	23	824.5	28.8	551	9	CB614460	AMGNNUC:N
	24	810	28.3	643	6	CD619813	56070459H
	25	806	28.2	719	5	BU701949	UI-M-PI0-
	26	786	27.5	520	9	CG633232	OST352674
	27	772.5	27.0	769	7	CO432359	UI-M-HX0-
	28	760	26.6	1930	3	AK090358	Mus muscu
	29	756.5	26.5	788	3	CR629695	DKFZp469L
c	30	738.5	25.8	664	7	CF170010	B0821001-
	31	736.5	25.8	595	6	CD623530	56050848H
	32	734.5	25.7	743	7	CF741826	UI-M-HB0-
	33	719	25.1	692	7	CN459174	UI-M-HN0-
	34	709.5	24.8	580	7	CF168714	B0803E12-
	35	709	24.8	421	5	BY218603	BY218603
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	37	697.5	24.4	3583	2	BP293170	60309806
	38	685	24.0	582	5	AK043875	Mus muscu
	39	684	23.9	420	2	AW353152	34940 MAR
	40	683	23.9	440	2	BF850604	PM1-HN006
c	41	680.5	23.8	559	5	BP293707	BP293707
	42	663.5	23.2	580	5	BP378639	BP378639
	43	663.5	23.2	584	5	BP267436	BP267436-
	44	663	23.2	799	5	CO247237	AGENCOURT
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ALIGNMENTS

RESULT 1
AY404850

LOCUS   AY404850   2514 bp   DNA   linear   GSS 16-DEC-2003
DEFINITION Homo sapiens ADAMTS4 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY404850
VERSION   AY404850.1 GI:39760827
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2514)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED   14671302
REFERENCE   2 (bases 1 to 2514)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
     source   1..2514

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 20:28:25 ; Search time 806 Seconds
(without alignments)
5427.710 Million cell updates/sec

GenCore version 5.1.6
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Title: US-10-628-432-32
Perfect score: 2859
Sequence: 1 MSQTGSHPGRGLAGRWLWGA............DQLQDFNIPQAVDYKDDDDK 529

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2805	98.1	4192	16	US-10-247-685-1	Sequence 1, Appli
2	2804	98.1	2542	20	US-10-628-432-14	Sequence 14, Appl
3	2801	98.0	1561	19	US-10-358-283-33	Sequence 33, Appl
4	2801	98.0	1726	19	US-10-358-283-32	Sequence 32, Appl
5	2801	98.0	4307	18	US-10-191-997-121	Sequence 121, App
6	2801	98.0	4307	19	US-10-358-283-31	Sequence 31, Appl
7	2801	98.0	4307	20	US-10-628-432-4	Sequence 4, Appli
8	2801	98.0	4307	22	US-10-956-157-1373	Sequence 1373, Ap
9	2798	97.9	4307	10	US-09-946-374-316	Sequence 316, App
10	2798	97.9	4407	14	US-10-052-586-351	Sequence 351, App
11	2798	97.9	4407	15	US-10-174-590-351	Sequence 351, App
12	2798	97.9	4407	15	US-10-176-758-351	Sequence 351, App
13	2798	97.9	4407	15	US-10-175-737-351	Sequence 351, App
14	2798	97.9	4407	15	US-10-174-581-351	Sequence 351, App
15	2798	97.9	4407	15	US-10-176-483-351	Sequence 351, App
16	2798	97.9	4407	15	US-10-176-749-351	Sequence 351, App
17	2798	97.9	4407	15	US-10-176-914-351	Sequence 351, App
18	2798	97.9	4407	15	US-10-176-915-351	Sequence 351, App
19	2798	97.9	4407	15	US-10-173-706-351	Sequence 351, App
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22	2798	97.9	4407	15	US-10-176-482-351	Sequence 351, App
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30	2798	97.9	4407	15	US-10-174-582-351	Sequence 351, App
31	2798	97.9	4407	15	US-10-174-588-351	Sequence 351, App
32	2798	97.9	4407	15	US-10-175-739-351	Sequence 351, App
33	2798	97.9	4407	15	US-10-175-740-351	Sequence 351, App
34	2798	97.9	4407	15	US-10-175-743-351	Sequence 351, App
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37	2798	97.9	4407	15	US-10-176-747-351	Sequence 351, App
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45	2798	97.9	4407	15	US-10-173-695-351	Sequence 351, App

ALIGNMENTS

RESULT 1
US-10-247-685-1
; Sequence 1, Application US/10247685
; Publication No. US20030108998A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909D
; CURRENT APPLICATION NUMBER: US/10/247,685
; CURRENT FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 1
; LENGTH: 4192

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: November 11, 2005, 20:27:24 ; Search time 194 Seconds
4461.806 Million cell updates/sec
(without alignments)

Title:
Perfect score: 2859
Sequence: 1 MSQTGSHPGRGLAGRWLWGA..........DQLQDFNIPQAVDYKDDDDK 529

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters: 2405568
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Database : Issued_Patents_NA:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2805	98.1	4192	3	US-10-628-432-32	Sequence 1, Appli
2	2805	98.1	4192	4	US-09-122-126B-1	Sequence 1, Appl
3	2805	98.1	4192	4	US-09-634-286A-1	Sequence 14, Appl
4	1193	41.7	4676	3	US-09-247-685-1	Sequence 1, Appl
5	1189	41.6	3889	4	US-09-130-491-1	Sequence 1, Appli
6	1180	41.3	4858	3	US-09-568-559-1	Sequence 1, Appli
7	1097	38.4	2853	4	US-09-392-184-1	Sequence 1, Appli
8	1055	36.9	3706	3	US-10-009-332-2	Sequence 2, Appli
9	1050	36.7	2184	4	US-09-488-970B-58	Sequence 58, Appl
10	1046.5	36.6	2184	4	US-09-445-023A-13	Sequence 13, Appl
11	1011.5	35.4	3638	3	US-09-369-364A-8	Sequence 8, Appli
c 12	870	30.4	3126	3	US-09-392-184-7	Sequence 7, Appli

No.	Score		Match Length	DB	ID	Description
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15	828	29.0	3250	4	US-09-634-286A-14	Sequence 14, Appl
16	783.5	27.4	5804	3	US-10-247-685-14	Sequence 12, Appl
17	733	25.6	2625	3	US-09-369-364A-12	Sequence 14, Appl
18	717	25.1	6659	4	US-09-321-987B-1	Sequence 1, Appl
19	645.5	22.6	3218	4	US-09-369-364A-6	Sequence 6, Appl
20	643.5	22.5	5357	3	US-09-392-184-5	Sequence 5, Appli
21	636	22.2	739	3	US-09-369-364A-10	Sequence 10, Appl
22	592	20.7	2727	4	US-09-963-791-11	Sequence 11, Appl
23	592	20.7	1770	4	US-09-963-791-1	Sequence 1, Appl
c 24	578.5	20.2	3571	4	US-09-799-451-411	Sequence 411, App
25	574	20.1	3377	3	US-09-981-953A-3	Sequence 3, Appl
26	570	19.9	703	3	US-10-217-774-5	Sequence 5, Appl
27	559.5	19.6	1317	4	US-09-392-791-21	Sequence 21, Appl
28	559.5	19.6	2274	4	US-09-963-791-23	Sequence 23, Appli
29	556.5	19.5	3766	4	US-09-981-953A-1	Sequence 1, Appli
30	544.5	19.0	1524	4	US-09-963-791-9	Sequence 9, Appl
31	515.5	18.0	4042	3	US-10-217-774-5	Sequence 5, Appli
32	512	17.9	1071	4	US-09-963-791-19	Sequence 19, Appl
33	505.5	17.7	3675	4	US-09-930-872-1	Sequence 1, Appl
34	505.5	17.7	3675	4	US-09-930-872-3	Sequence 3, Appli
35	486.5	17.0	2450	3	US-10-217-774-3	Sequence 3, Appl
36	486.5	17.0	6692	4	US-09-491-522-2	Sequence 2, Appli
37	485.5	17.0	3636	4	US-09-949-016-5530	Sequence 5530, Ap
38	485.5	17.0	3160	4	US-09-963-791-25	Sequence 25, Appl
39	482.5	16.9	3160	4	US-09-963-791-25	Sequence 25, Appl
40	479.5	16.8	2450	4	US-09-491-522-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-09-122-126B-1

; Sequence 1, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
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; SEQ ID NO 1
; LENGTH: 4192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
;
US-09-122-126B-1

Alignment Scores:
Pred. No.:   8.58e-239
Score: 2805.00
Percent Similarity: 100.00%   Length: 4192
Best Local Similarity: 99.81%   Matches: 519
Query Match: 98.11%   Conservative: 1
                                       Mismatches: 1
                                       Indels: 0
                                       Gaps: 0

DB: US-09-122-126B-1

US-10-628-432-32 (1-529) x US-09-122-126B-1 (1-4192)

Qy   1 MetSerGlnThrGlySerHisProGlyArgGlyLeuAlaGlyArgTrpLeuTrpGlyAla   20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 406 ATGTCCCAGACAGGCTCGCATCCCGGAGGGGGGCTTGGCAGGGCGCTGGCTGTGGGGAGCC 465

Qy   21 GlnProCysLeuLeuLeuProIleValProLeuSerTrpLeuValTrpLeuLeuLeuLeu   40

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: November 11, 2005, 19:59:59 ; Search time 555 Seconds
(without alignments)
5642.420 Million cell updates/sec

Title: US-10-628-432-32
Perfect score: 2859
Sequence: 1 MSQTGSHPGRGLLAGRWLWGA.........DQLQDFNIPQAVDYKDDDDK 529

Scoring table: BLOSUM62
Xgapext   0.5
Xgapop   10.0 ,   Xgapext   0.5
Ygapop   10.0 ,   Ygapext   0.5
Fgapop   6.0 ,   Fgapext   7.0
Delop   6.0 ,   Delext   7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10628432/runat 03112005 080225 14117/app_query.fasta_1.711
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCOR=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10628432 @CGN_1_1_470 @runat 03112005 080225 14117 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY _NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_16Dec04:*
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2:    geneseqn1909s:*
3:    geneseqn2008s:*
4:    geneseqn2001as:*
5:    geneseqn2001bs:*
6:    geneseqn2002as:*
7:    geneseqn2002bs:*
8:    geneseqn2003as:*
9:    geneseqn2003bb:*
10:    geneseqn2003cs:*
11:    geneseqn2003bs:*
12:    geneseqn2004as:*
13:    geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	2805	98.1	4192	2	AAX00725	Aax00725 Human agg
2	2804	98.1	2542	13	ADS20217	Ads20217 Human agg
3	2801	98.0	1560	10	ADB85506	Adb85506 Human agg
4	2801	98.0	1725	10	ADB85505	Adb85505 Human agg
5	2801	98.0	2514	10	ADL13488	Adl13488 Osteoarth
6	2801	98.0	4301	4	AAI68146	Aai68146 Human agg
7	2801	98.0	4301	10	ADL13487	Adl13487 Osteoarth
8	2801	98.0	4303	3	AAA95826	Aaa95826 Human met
9	2801	98.0	4307	10	ADB85504	Adb85504 Human agg
10	2801	98.0	4307	10	ACF63399	Acf63399 Human ADA
11	2801	98.0	4307	13	ADS20212	Ads20212 Human agg
12	2798	97.9	4406	4	ACA89550	Aca89550 cDNA enco
13	2798	97.9	4407	4	ACA73560	Aca73560 Human sec
14	2798	97.9	4407	8	AAA37111	Aaa37111 Human sec
15	2798	97.9	4407	4	AAF54426	Aaf54426 Probe #46
16	2798	97.9	4407	10	AAA46100	Aaa46100 Human DNA
17	2798	97.9	4407	4	ACA05875	Aca05875 Human sec
18	2798	97.9	4407	8	ACA66709	Aca66709 cDNA enco
19	2798	97.9	4407	8	ACF20284	Acf20284 Human sec
20	2798	97.9	4407	8	ACF19670	Acf19670 Human sec
21	2798	97.9	4407	8	ACD21958	Acd21958 Human sec
22	2798	97.9	4407	8	ACF13123	Acf13123 Human sec
23	2798	97.9	4407	8	ACD25226	Acd25226 Human sec
24	2798	97.9	4407	8	ACF00275	Acf00275 Human sec
25	2798	97.9	4407	8	ACA72332	Aca72332 Novel hum
26	2798	97.9	4407	8	ACD04856	Acd04856 Novel hum
27	2798	97.9	4407	8	ACD18317	Acd18317 Human sec
28	2798	97.9	4407	8	ACD08324	Acd08324 Human sec
29	2798	97.9	4407	8	ACA88758	Aca88758 Novel hum
30	2798	97.9	4407	8	ACA70200	Aca70200 Novel hum
31	2798	97.9	4407	8	ACD12422	Acd12422 Novel hum
32	2798	97.9	4407	8	ACC74337	Acc74337 Human sec
33	2798	97.9	4407	8	ACD15965	Acd15965 Human sec
34	2798	97.9	4407	8	ACD25533	Acd25533 Human sec
35	2798	97.9	4407	8	ACD18010	Acd18010 Novel hum
36	2798	97.9	4407	8	ACC88297	Acc88297 Human sec
37	2798	97.9	4407	8	ACD21651	Acd21651 Human sec
38	2798	97.9	4407	8	ACD18718	Acd18718 Human sec
39	2798	97.9	4407	8	ABX98328	Abx98328 Human sec
40	2798	97.9	4407	8	ACD14079	Acd14079 Human PRO
41	2798	97.9	4407	8	ACD09859	Acd09859 Human PRO
42	2798	97.9	4407	8	ACC88604	Acc88604 Human sec
43	2798	97.9	4407	8	ACD21344	Acd21344 Human sec
44	2798	97.9	4407	8	ABX75716	Abx75716 Human CDN
45	2798	97.9	4407	8	ABX97919	Abx97919 Human PRO

ALIGNMENTS

RESULT 1
AAX00725

ID   AAX00725 standard; cDNA to mRNA; 4192 BP.
XX
AC   AAX00725;
XX
DT   30-MAR-1999   (first entry)
XX
DE   Human aggrecan degrading metalloprotease 1 gene.
XX
KW   Human; aggrecan degrading metalloprotease; cartilage; proteoglycan;
KW   interglobular domain; matrix metalloprotease; bovine; interleukin-1beta;
KW   primer; PCR; amplification; inhibitor; cleavage; inhibitor; ADMP; ss;
KW   arthritis; joint injury; pseudogout.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   406..2919
FT   /*tag= a
FT   /product= "ADMP-1"
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XX
PN   WO9905291-A2.
XX
PD   04-FEB-1999.
XX
PF   24-JUL-1998; 98WO-US015438.
XX

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: November 11, 2005, 20:15:59 ; Search time 4498 Seconds
                                            (without alignments)
                                            5698.713 Million cell updates/sec

Title:
Perfect score: 2859
Sequence: 1 MSQTGSHPGRGLAGRWLWGA...........DQLQDFNIPQAVDYKDDDDK 529

Scoring table:
                US-10-628-432-32

                BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop   6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10628432//runat_03112005_080225_14127/app_query.fasta_1.711
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=1 -THREADS=1 -XGAPOP=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=100 -LONGLOG
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7   -XGAPEXT=0.5 -FGAPOP=6

Database :   GenEmbl:*
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                2:   gb_htg:*
                3:   gb_in:*
                4:   gb_om:*
                5:   gb_ov:*
                6:   gb_pat:*
                7:   gb_ph:*
                8:   gb_pl:*
                9:   gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*

                                    SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query % Match	Length DB	ID	Description
1	2805	98.1	4192	6	AR230264	AR230264 Sequence
2	2805	98.1	4192	6	AR282324	AR282324 Sequence
3	2805	98.1	4192	6	AR560177	AR560177 Sequence
4	2805	98.1	4192	6	BD073443	BD073443 Aggrecan-

5	2805	98.1	4193	9	AF148213	AF148213 Homo sapi
6	2801	98.0	4301	6	BD016729	BD016729 Promoter
7	2801	98.0	4301	6	AB014588	AB014588 Homo sapi
8	2798	97.9	4407	6	AX376284	AX376284 Sequence
9	2798	97.9	4407	6	AX697248	AX697248 Sequence
10	2798	97.9	4407	6	AY358886	AY358886 Homo sapi
11	2790	97.6	4341	9	BC063293	BC063293 Homo sapi
12	2777	97.1	2317	6	CQ716637	CQ716637 Sequence
13	2459	86.0	3720	4	AF516915	AF516915 Bos tauru
14	2459	86.0	3321	6	BC027773	BC027773 Homo sapi
15	2427.5	84.9	4281	10	AK173001	AK173001 Mus muscu
16	2170	75.9	167863	2	AL590651	AL590651 Mus muscu
17	2151.5	75.3	133512	9	AL590714	AL590714 Human DNA
18	2147.5	75.1	10766	9	AY044847	AY044847 Homo sapi
19	1830	64.0	1991	10	BC030812	BC030812 Homo sapi
20	1655.5	57.9	211776	10	AC084821	AC084821 Mus muscu
21	1655.5	57.9	227141	2	AC093409	AC093409 Mus muscu
22	1593	55.7	1251	10	AB042271	AB042271 Rattus no
23	1593	55.7	1878	6	BD094440	BD094440 Novel gen
24	1227	42.9	4180	6	BD129556	BD129556 Polynucle
25	1227	42.9	4180	10	D67076	D67076 Mouse mRNA
26	1223	42.8	3943	10	BC040382	BC040382 Mus muscu
27	1223	42.8	4909	10	BC050834	BC050834 Mus muscu
28	1222	42.7	2871	9	AX577901	AX577901 Sequence
29	1221.5	42.7	4878	10	AF149118	AF149118 Rattus no
30	1220.5	42.7	4395	10	BC080237	BC080237 Rattus no
31	1203	42.1	2857	10	AF304446	AF304446 Rattus no
32	1193	41.7	2853	6	E58656	E58656 Novel metal
33	1193	41.7	3261	6	BD129546	BD129546 Polynucle
34	1193	41.7	3430	6	AX577976	AX577976 Sequence
35	1193	41.7	3430	6	AF060152	AF060152 Homo sapi
36	1193	41.7	4014	9	E29406	E29406 Novel integ
37	1193	41.7	4309	6	AB037767	AB037767 Homo sapi
38	1193	41.7	4665	9	BC036515	BC036515 Homo sapi
39	1193	41.7	4676	6	AR217550	AR217550 Sequence
40	1193	41.7	4676	6	BD080292	BD080292 Tango-71,
41	1191	41.7	4447	9	AF170084	AF170084 Homo sapi
42	1189	41.6	3889	10	AR430581	AR430581 Sequence
43	1189	41.6	4659	9	AF207664	AF207664 Homo sapi
44	1186.5	41.5	4666	9	BX647388	BX647388 Homo sapi
45	1181	41.3	4712	6	BD194902	BD194902 86 human

                                    ALIGNMENTS

RESULT 1
AR230264

LOCUS   AR230264   4192 bp   DNA   linear   PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6451575.
ACCESSION   AR230264
VERSION   AR230264.1   GI:27270379
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 4192)
  AUTHORS   Arner,E.C., Burn,T.C., Copeland,R.A., Decicco,C.P., Liu,R.,
            Magolda,R., Pratta,M., Solomon,K.A., Tortorella,M.D., Trzaskos,J.M.
            and Yang,F.
  TITLE   Aggrecan degrading metallo proteases
  JOURNAL   Patent: US 6451575-A 1 17-SEP-2002;
FEATURES   Location/Qualifiers
     source   1..4192
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:   7.76e-134
Score: 2805.00
Percent Similarity: 100.00%
Best Local Similarity: 1..4192
Query Match: 98.11%

Length:	4192	
Matches:	519	
Conservative:	1	
Mismatches:	0	
Indels:	0	